



FIGURE 12

TAT	ATC	GAG	CGG	GAT	GTG
Y	I	E	R	D	V
GTC	CAT	CGC	ACT	AAC	TTC
V	H	R	T	N	
603	549	495	441	387	333
ATC	GAC	ATC	CAG	TTC	GCC
I	D	I	Q	F	A
GAA E	TTC	AAC N	ATG M	TTC	TCT
CTC	CAG	GTG	GAG	CGC	GTC
	Q	V	E	R	V
612	558	504	450	396	342
AAC	CGG	CCT	CTG	TGT	TAC
N	R	P	L	C	Y
ACC T	GGT	GTG V	GAA E	GGT	ATC I
ACC	CTG	P	GAG	GTG	TAC
T		CCC	E	V	Y
621	567	513	459	405	351
ATT	ACT	CAG	GAT	CTG	AGA
I	T	Q	D	L	R
GTG	GCG	TTT	GTG	TAT	TAC
V	A	F	V	Y	Y
CTG	TAC Y	G G	AAA K	GAG E	TTC
630 CCC	576 CAT H	522 GGC G	468 ATC I	414 GAC D	360 TTT F
P	GAT D	GGT	TAC Y	TCC	CTT
CGC	ATC I	GAC D	CTC	CTG L	GCA A
639	585	531	47.7	423	369
AAC	TTG	CCT	GAC	TCC	CAG
N	L	P	D	S	Q
TTC	GAC D	GCA A	GAG E	TCC	CTG
648 TTC TGG GAG F W E	594 GAC AAG TGC D K C	540 GCA GAC ATC A D I	AAC N	CAG Q	GCC A
648	594	540	486	432	378
GAG	TGC	ATC	GAG AAC TAC	CAG GTC	CTG GCC CGA
E	C	I	E N Y	Q V	L A R

FIGURE 1B

222	GAG E	CGG R	ATC I	GAG E	CTC
	) AAC	3 AGG R	TAC	G GAG	T C CTC
927 CCA GAA	873 ACC T	819 CGG R	765 CAC H	711 ATG	657 ATG
ccc	TTC F	ATC I	CTG	GTG V	AAC N
CCT	GTG V	AAC	TGC C	GTC V	GTG V
936 GCC	882 GTG V	828 AAG K	774 AAC N	720 ACG T	666 AAG K
GTG	GAG E	CGT	GGG G	GAG E	AGG R
TTC	ACG T	G G	AAA K	CAT H	GGG G
945 CTC	891 CTC L	837 GCC A	783 GAC D	729 GTC V	675 ACC T
TTT	ATC I	AAG K	ACC T	AGT S	TAC Y
TCT	TGC C	AAC N	TAC Y	GAC D	L
954 TCT	900 GGG G	846 TGC C	792 CGG R	738 AAG K	684 CCG P
TTC	GTG V	AAT N	CTC	GAG E	CAG Q
CGG	GTG V	GCC A	CGG R	GCC A	ACG T
963 CTG	909 TGA	855 ATC	801 CGC R	747 CTG L	693 TAC Y
CTC	GGC	CGC R	CGG R	GGG	ATC I
972 CTC TCT GGC	918 CCT CCT	CGC CAC	810 CGG GCA ACG R A T	TCC	ATC I
972 GGC	918 CCT	864 TTC F	810 ACG T	756 G S F	702 ATC ATC CAG I I Q

FIGURE 1C

TCT CTC GGT GGG GGG CCC ATC TCT GCT GAC CTG GGT GTG GCG GAG GGA GAG GCG CAT GTC TCT CCA TTC CTC TCC AAC CCT GCC CAC CTC CCT GTA CCA GAG CTG TGA 990 999 1008 1017 1026 CCT CCT TCC CCC TGC TTA GCT TGT ACT TTG GAC GCG TTT CTA TAG AGG TGA P P P S P C L A C T T T T T T T 

FIGURE 1D

ATG CTG CAA AGT GTT TTC TGT GTC CCA CTG TCT TGA AGC TGG GCC TGC

- MV MVKIAFNTPTAVQKEE × വ μ OPAVAGI KGDKADKASAS 1 1 × Ħ QDIE APAPASATEILLTPAR ALVS RTVRAQILTGKE GI 624778 662708
- 39 ۲ RVVPOEK-H 0 P \_ קי QHRS KRGGSVGGVCYLSM-GMVVLLMGLVFASVY---DGSSGRCMLTLLGLSFILAGLIVGGAC GACL GI 624778 662708
- 8 % YRYFF YKYF-H ı AOL z ש ≫ X S RDNF Н Н НА FRCGVLY - - -G Ħ MC H Ή D S [Ŧ] H U D PVN SIS S SOVRTO IPGGEPYFLP I I -М Е 662708

GI 624778

- 111 114 LEEDVKIYLDENYERINVPVPS POFGGGDPADIIHDFORGLT PSFSDSDPAAIIHDFEKGMT GI 624778 662708
- 151 154 AYHDIL-DKCYVIELNTTIVLPPRNEWELLMNVKRGTYLP AYLDLLLGNCYLMPLNTSIVMTPKNLVELFGKLASGKYLP 662708 GI 624778
- 191 193 OTYIIOEEMVVTEHVSD HTYVVREDLVAVEEIRD HVSDKEALGSFIYHLC EIRDVSNLGIFIYQLC LCNNRKS NGKDTYRL ļτj RLRRR æ R R GI 624778 662708
- 231 233 ATRRRI U Ľ RRRINKRGAKNCNAIRHFENTFVVETLICGVV LLGFNKRAIDKCWKIRHFPNEFIVETKICQE

GI 624778

662708

## FIGURE 2